Cont B1

BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.--

Please replace the paragraph beginning at page 13, line 12 with the following rewritten paragraph:

--Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be obtained from the National Institute of Health, Bethesda, MD. NCBI-

B2

BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.--

Please replace the paragraph beginning at page 65, line 15 with the following rewritten paragraph:

--The extracellular domain (ECD) sequences (including the secretion signal, if any) of from about 950 known secreted proteins from the Swiss-Prot public protein database were used to search expressed sequence tag (EST) databases. The EST databases included public EST databases (e.g., GenBank) and a

B3

proprietary EST DNA database (LIFESEQ^{TM}, Incyte Pharmaceuticals, Palo Alto, CA). The search was performed using the computer program BLAST or BLAST2 (Altshul et al., Methods in Enzymology 266:460-480 (1996)) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequence. Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, Washington).--

In the claims:

Please amend Claims 15, 16, 17, 19, 27, 29-31 to read as follows, and add new Claim 47. Please cancel Claim 21.

B4 15. (Twice amended) An isolated Bolekine polypeptide comprising amino acid residues 1 to 111 of ~~Figure 2 (SEQ ID NO:2).~~

16. (Amended) An isolated Bolekine polypeptide which is encoded by the cDNA insert of the vector B5 deposited with the ATCC on October 31, 1997 as ATCC Deposit No. 209424 (DNA39523-1192).

17. (Amended) An isolated Bolekine polypeptide comprising the sequence of amino acids from 1 to 111 of Figure 2 (SEQ ID NO:2), or a fragment thereof, wherein said fragment is capable of enhancing the proliferation of T lymphocytes in a mammal.

19. (Amended) A chimeric molecule comprising the Bolekine polypeptide as in Claim 17, fused to B6 a heterologous amino acid sequence.

27. (Amended) A composition of matter comprising the Bolekine polypeptide as in Claim 17, in B7 admixture with a pharmaceutically acceptable carrier.

29. (Amended) The composition of matter of Claim 27, wherein the Bolekine polypeptide is capable of (i) enhancing the proliferation of T-lymphocytes in a mammal, or (ii) increasing infiltration of B8 inflammatory cells into a tissue of a mammal.

30 (Amended) The composition of matter of Claim 27 comprising a therapeutically effective amount of the Bolekine polypeptide.

31 (Amended) An article of manufacture, comprising:

a container;

a label on said container; and

a composition of matter comprising a Bolekine polypeptide of Claim 17, contained within said container, wherein label on said container indicates that said composition of matter can be used for treating an immune related disease.

--47 (new) An isolated Bolekine polypeptide comprising amino acid residues 34 to 111 of Figure 2 B9 (SEQ ID NO:2). --